



SEQUENCE LISTING

<110> Jensen, Michael

<120> Selection Systems for Genetically Modified Cells

<130> 24751-2502

<140> US/09/846,637

<141> 2001-04-30

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<223> Human Wild-type Inosine Monophosphate Dehydrogenase II (IMPDH II)

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<301> Collart, F.R. and Huberman, E.

<302> Cloning and sequence analysis of the human and

<303> J. Biol. Chem. (1988)

<304> 263

<306> 15769-15772

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1654

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<300>
 <301> Parazi et al.
 <303> J. Biol. Chem. (1997)
 <304> 271
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 <301> Farazi et al.
 <303> J. Biol. Chem. (1997)
 <304> 272
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Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile																
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 <301> Farazi et al.
 <303> J. Biol. Chem. (1997)
 <304> 272
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Gln Thr Phe Ala Asp Val Leu Ala Ile Ser Gln Arg Thr Thr His Asn	
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His	Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys	
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Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
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cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg	336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
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Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr	
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Ans

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<300>  
<301> Natsumeda et al.  
<302> Two Distinct cDNAs for Human IMP Dehydrogenase  
<303> J. Biol. Chem. (1990)  
<304> 265  
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 <301> Minet, M., Dufour, M-E., and Lacroute, F.
 <302> Cloning and Sequencing of a Human cDNA coding for
 <303> Gene (1992)
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Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala	Ser	Leu	
			340					345					350			
gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	gtt	gtg	ggc	1104
Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val	Val	Gly	
		355					360					365				

aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag ggc ttt ggc	1152
Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly	
370 375 380	

gga gtc aca gat gcc att gga gca gat cat cgg agg tgaggacagc	1198
Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg	
385 390 395	

gtctgacggg aagcctgatac tggaaccttc ccaaggactc aggcaagcct ttgtggctgg	1258
atcatgagag gagggactcc atcttgagcc atgtcccccga gcctggcatg cgtgcactgt	1318
aaacgccaat cgggggggtca ccaggatcaa ccgcaggctt tcttcagtcct cttgggtcaga	1378
ccataaactg catttttgat tctttgtgga ttcaaaccct aggatccatc agtcttgcaa	1438
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 <211> 396
 <212> PRT
 <213> Homo Sapien

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Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly	
35 40 45	
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser	
50 55 60	
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu	
65 70 75 80	
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala	
85 90 95	
Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly	
100 105 110	
Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly	
115 120 125	
Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile	
130 135 140	
Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg	
145 150 155 160	
Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu	
165 170 175	
Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala	
180 185 190	
Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr	
195 200 205	
Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu	
210 215 220	
Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu	
225 230 235 240	
Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile	
245 250 255	
Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val	
260 265 270	
Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser	
275 280 285	
Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu	
290 295 300	
Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met	
305 310 315 320	
Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val	
325 330 335	
Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu	
340 345 350	
Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly	
355 360 365	
Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly	

Q14
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Ala	Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	
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cgg	agc	ctt	cag	gga	aag	gcc	gag	ctg	cgc	cgc	ctg	ctg	acc	aag	gtg	624
Arg	Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	
		195					200					205				
ctg	cag	gag	agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	672
Leu	Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	
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gtg	aag	atc	gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	720
Val	Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	
225					230				235						240	
agt	gtg	gtc	aaa	gag	ttg	ggc	atc	gat	ggg	ctg	att	gtt	acg	aac	acc	768
Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	
				245					250					255		
acc	gtg	agt	cgc	cct	gcg	ggc	ctc	cag	ggc	ctg	cgc	tct	gaa	aca		816
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	
			260					265					270			

gga	ggg	ctg	agt	ggg	aag	ccc	ctc	cgg	gat	ttg	tca	act	caa	acc	att	884
Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	
		275					280					285				
cgg	gag	atg	tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	912
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	
	290					295					300					
ggt	ggt	gtg	agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	960
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	
305					310				315						320	
gcc	tcc	ctg	gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	1008
Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	
				325				330						335		
gtt	gtg	ggc	aaa	gtc	aag	cgg	gaa	ctg	gag	gcc	ctt	ctg	aaa	gag	cag	1056
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln	
			340				345						350			
ggc	ttt	ggc	gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg		1101
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<210> 22
 <211> 367
 <212> PRT
 <213> Homo sapien

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 Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
 35 40 45
 Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
 50 55 60
 Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
 65 70 75 80
 Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
 85 90 95
 Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln

Ala	Val	Ile	100	Asn	Arg	Tyr	Gly	Phe	105	Asn	Ser	His	Gly	Leu	110	Ser	Val	Val
			115						120						125			
Glu	His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu			
			130						135						140			
Asp	Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val			
145						150						155			160			
Asp	Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu			
				165						170					175			
Ala	Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu			
			180							185					190			
Arg	Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val			
			195					200							205			
Leu	Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu			
			210				215					220						
Val	Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala			
225					230					235					240			
Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr			
				245					250						255			
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr			
			260						265						270			
Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile			
			275				280						285					

Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val			
			290				295					300						
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly			
305					310					315					320			
Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro			
				325					330						335			
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln			
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<210> 23
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<220>
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<221> mutation
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 <223> His26Ala DHODH mutant

<300>
 <301> Davis et al.
 <302> Histidine to Alanine mutants of Human Dihydroorota
 <303> Biochem. Pharmacol. (1997)
 <304> 54
 <306> 459-465

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	Ala	Thr	Gly	Asp	Glu	Arg	Phe	Tyr	Ala	Glu	His	Leu	Met	Pro	Thr			
	1				5				10						15			
ctg	cag	ggg	ctg	ctg	gac	ccg	gag	tca	gcc	gcc	aga	ctg	gct	gtt	cgc			96
Leu	Gln	Gly	Leu	Leu	Asp	Pro	Glu	Ser	Ala	Ala	Arg	Leu	Ala	Val	Arg			
				20					25					30				

ttc	acc	tcc	ctg	ggg	ctc	ctt	cca	cgg	gcc	aga	ttt	caa	gac	tct	gac	144
Phe	Thr	Ser	Leu	Gly	Leu	Leu	Pro	Arg	Ala	Arg	Phe	Gln	Asp	Ser	Asp	
			35					40					45			
atg	ctg	gaa	gtg	aga	gtt	ctg	ggc	cat	aaa	ttc	cga	aat	cca	gta	gga	192
Met	Leu	Glu	Val	Arg	Val	Leu	Gly	His	Lys	Phe	Arg	Asn	Pro	Val	Gly	
		50					55					60				
att	gct	gca	gga	ttt	gac	aag	cat	ggg	gaa	gcc	gtg	gac	gga	ctt	tat	240
Ile	Ala	Ala	Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	
	65					70					75					
aag	atg	ggc	ttt	ggg	ttt	gtt	gag	ata	gga	agt	gtg	act	cca	aaa	cct	288
Lys	Met	Gly	Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	
80					85					90					95	
cag	gaa	gga	aac	cct	aga	ccc	aga	gtc	ttc	cgc	ctc	cct	gag	gac	caa	336
Gln	Glu	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	
				100					105					110		
gct	gtc	att	aac	agg	tat	gga	ttt	aac	agt	cac	ggg	ctt	tca	gtg	gtg	384
Ala	Val	Ile	Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	
			115					120				125				
gaa	cac	agg	tta	cgg	gcc	aga	cag	cag	aag	cag	gcc	aag	ctc	aca	gaa	432
Glu	His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	
		130					135					140				
gat	gga	ctg	cct	ctg	ggg	gtc	aac	ttg	ggg	aag	aac	aag	acc	tca	gtg	480
Asp	Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	
	145					150					155					
gac	gcc	gcg	gag	gac	tac	gca	gaa	ggg	gtg	cgc	gta	ctg	ggc	ccc	ctg	528
Asp	Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	
160					165					170					175	
gcc	gac	tac	ctg	gtg	gtg	aat	gtg	tcc	agc	ccc	aac	act	gcc	ggg	ctg	576
Ala	Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	
				180					185					190		
cgg	agc	ctt	cag	gga	aag	gcc	gag	ctg	cgc	cgc	ctg	ctg	acc	aag	gtg	624
Arg	Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	
			195				200						205			
ctg	cag	gag	agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	672
Leu	Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	
		210					215					220				
gtg	aag	atc	gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	720
Val	Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	
	225					230					235					
agt	gtg	gtc	aaa	gag	ttg	ggc	atc	gat	ggg	ctg	att	gtt	acg	aac	acc	768
Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	
240					245					250					255	
acc	gtg	agt	cgc	cct	gcg	ggc	ctc	cag	ggg	gcc	ctg	cgc	tct	gaa	aca	816
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	
				260					265					270		
gga	ggg	ctg	agt	ggg	aag	ccc	ctc	cgg	gat	tta	tca	act	caa	acc	att	864
Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	
			275					280					285			
cgg	gag	atg	tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	912
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	

290					295					300						
ggt	ggt	gtg	agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	960
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	
	305					310					315					
gcc	tcc	ctg	gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	1008
Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	
	320				325					330					335	
gtt	gtg	ggc	aaa	gtc	aag	cgg	gaa	ctg	gag	gcc	ctt	ctg	aaa	gag	cag	1056
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln	
				340					345					350		
ggc	ttt	ggc	gga	gtc	aca	gat	gcc	att	gga	gca	gat	cat	cgg	agg		1101
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<210> 24
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 <212> PRT
 <213> Homo sapien

<400> 24

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Gln	Gly	Leu	Leu	Asp	Pro	Glu	Ser	Ala	Ala	Arg	Leu	Ala	Val	Arg	Phe
		20						25					30		
Thr	Ser	Leu	Gly	Leu	Leu	Pro	Arg	Ala	Arg	Phe	Gln	Asp	Ser	Asp	Met
		35					40					45			
Leu	Glu	Val	Arg	Val	Leu	Gly	His	Lys	Phe	Arg	Asn	Pro	Val	Gly	Ile
	50					55					60				
Ala	Ala	Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	Lys
65					70					75					80
Met	Gly	Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	Gln
				85					90					95	
Glu	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	Ala
			100					105					110		
Val	Ile	Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	Glu
		115					120					125			
His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	Asp
	130					135					140				
Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	Asp
145					150					155					160
Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	Ala
				165					170					175	
Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg
			180					185					190		
Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu
		195					200						205		
Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val
	210					215					220				
Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser
225					230					235					240
Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr
				245					250					255	
Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	Gly
			260					265					270		
Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	Arg
		275					280					285			
Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	Gly
	290					295					300				
Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala
305					310					315					320
Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val
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atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag 576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
180 185 190

gat Asp	ggt Gly	aac Asn 195	ccg Pro	cgt Arg	cct Pro	cgc Arg	gaa Glu 200	ttc Phe	cga Arg	ctt Leu	cca Pro	tca Ser 205	cag Gln	aga Arg	gcg Ala	624
atg Met	ata Ile 210	aac Asn	cgg Arg	tac Tyr	ggc Gly	ctc Leu 215	aac Asn	tcc Ser	aaa Lys	ggc Gly	gca Ala 220	gat Asp	cac His	atg Met	gca Ala	672
gct Ala 225	atc Ile	ttg Leu	gag Glu	caa Gln	cga Arg 230	gta Val	cgc Arg	gat Asp	ttt Phe	gcc Ala 235	tac Tyr	gca Ala	aac Asn	gga Gly	ttt Phe 240	720
ggg Gly	gca Ala	tac Tyr	gat Asp	gcg Ala 245	gct Ala	aag Lys	cag Gln	cgt Arg	gta Val 250	ttg Leu	gac Asp	ggc Gly	gaa Glu	gct Ala 255	ggt Gly	768
gtg Val	cca Pro	cca Pro	ggt Gly 260	agt Ser	ctt Leu	cag Gln	cct Pro	ggt Gly 265	aag Lys	ctt Leu	tta Leu	gct Ala	gtc Val 270	caa Gln	gtg Val	816
gca Ala	aag Lys	aac Asn 275	aag Lys	gcc Ala	act Thr	cct Pro	gac Asp	ggc Gly	gac Asp	att Ile	gaa Glu	gcc Ala 285	atc Ile	aag Lys	cgc Arg	864
gac Asp	tat Tyr 290	gtg Val	tat Tyr	tgc Cys	gtg Val	gac Asp 295	cgt Arg	gtg Val	gcc Ala	aaa Lys	tac Tyr 300	gct Ala	gat Asp	att Ile	ctt Leu	912
gtt Val 305	gtg Val	aat Asn	gta Val	tcg Ser	agc Ser 310	ccc Pro	aac Asn	aca Thr	ccc Pro	ggc Gly 315	ctc Leu	cgt Arg	gac Asp	ctt Leu	caa Gln 320	960
gcc Ala	act Thr	gcc Ala	ccg Pro	ctc Leu 325	aca Thr	gct Ala	atc Ile	ttg Leu	agt Ser 330	gct Ala	gtc Val	gtt Val	ggc Gly	gcg Ala 335	gca Ala	1008
aag Lys	agc Ser	gtg Val	aac Asn 340	cgc Arg	aag Lys	acc Thr	aaa Lys	cca Pro 345	tat Tyr	gtt Val	atg Met	gtc Val	aag Lys 350	gtc Val	agt Ser	1056
ccg Pro	gat Asp	gaa Glu 355	gac Asp	tca Ser	gat Asp	gaa Glu	caa Gln 360	gtc Val	tct Ser	ggc Gly	atc Ile	tgc Cys 365	gac Asp	gcc Ala	gtc Val	1104
cga Arg 370	gca Ala	tcc Ser	ggt Gly	gtc Val	gac Asp	gga Gly 375	gtg Val	att Ile	gtc Val	gga Gly	aac Asn 380	aca Thr	aca Thr	aac Asn	cgt Arg	1152
cgc Arg 385	ccc Pro	gac Asp	cct Pro	ata Ile	ccc Pro 390	caa Gln	ggc Gly	tac Tyr	act Thr	ctt Leu 395	ccg Pro	gcc Ala	aag Lys	gag Glu	cag Gln 400	1200
gca Ala	acg Thr	ttg Leu	aaa Lys	gaa Glu 405	acc Thr	ggc Gly	ggg Gly	tat Tyr	tca Ser 410	ggc Gly	cca Pro	cag Gln	ctg Leu	ttc Phe 415	gat Asp	1248
cgc Arg	aca Thr	gtg Val	gcc Ala 420	ctt Leu	gtg Val	gct Ala	cgg Arg	tac Tyr 425	cgc Arg	tcc Ser	atg Met	ctg Leu	gat Asp 430	gcg Ala	gag Glu	1296
tcg Ser	gaa Glu	acg Thr 435	gcc Ala	gga Gly	tcc Ser	gcc Ala	aag Lys 440	gat Asp	tca Ser	gca Ala	gcg Ala	acc Thr 445	ata Ile	gcg Ala	caa Gln	1344
aca Thr	gag Glu	cca Pro	ggc Gly	tcg Ser	gaa Glu	aac Asn	gtt Val	cct Pro	cct Pro	gtg Val	gaa Glu	gcg Ala	cca Pro	agc Ser	gga Gly	1392

450		455		460	
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag					1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys					
465		470		475	480
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac					1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr					
		485		490	495
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa					1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln					
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gaa ctt cga acg gcg aaa aag gag					1560
Glu Leu Arg Thr Ala Lys Lys Glu					
		515		520	

<210> 26
 <211> 520
 <212> PRT
 <213> *Aspergillus nidulans*

<400> 26

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Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu	
35 40 45	
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
50 55 60	
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
65 70 75 80	
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
85 90 95	
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
100 105 110	
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
115 120 125	
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
130 135 140	
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
145 150 155 160	
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
165 170 175	
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	
180 185 190	
Asp Gly Asn Pro Arg Pro Arg Glu Phe Arg Leu Pro Ser Gln Arg Ala	
195 200 205	
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
210 215 220	
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	
245 250 255	
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	
260 265 270	
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg	
275 280 285	
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu	
290 295 300	
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln	
305 310 315 320	
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala	
325 330 335	

Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
			340					345					350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
		355					360					365			
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
	370					375					380				
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
	385				390					395					400
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
				405				410						415	
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
			420					425					430		
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
		435					440					445			
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
	450					455					460				
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
	465				470					475					480
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
			485					490					495		
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
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Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								

<210> 27
 <211> 1560
 <212> DNA
 <213> Aspergillus nidulans

 <220>
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 <222> (1)...(1560)
 <223> Aspergillus nidulans Ala115Val mutant DHODH cDNA

 <221> mutation
 <222> 344
 <223> C to T mutation

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1				5				10						15		
ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc																96
Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe	
			20					25					30			
gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa																144
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
		35					40					45				
tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag																192
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys	
	50					55					60					
gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg																240
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu	
	65				70					75					80	
acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg																288
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val	
				85				90						95		
cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg																336
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala	
			100					105					110			

gaa Glu	gat Asp	gtg Val 115	cat His	cat His	att Ile	ggt Gly	gtc Val 120	gat Asp	act Thr	tta Leu	aag Lys	atg Met 125	ctg Leu	tat Tyr	aag Lys	384
tat Tyr	ggt Gly 130	ctg Leu	cat His	cca Pro	agg Arg	gaa Glu 135	cgg Arg	ggg Gly	gat Asp	ccg Pro	gat Asp 140	gga Gly	gat Asp	ggg Gly	gcg Ala	432
ctg Leu 145	gcg Ala	aca Thr	gag Glu	gtc Val	ttt Phe 150	ggg Gly	tat Tyr	aca Thr	ctg Leu	tca Ser 155	aac Asn	cca Pro	att Ile	ggc Gly	ata Ile 160	480
tcg Ser	ggc Gly	ggc Gly	ctg Leu	gac Asp 165	aag Lys	cat His	gct Ala	gag Glu	atc Ile 170	cct Pro	gat Asp	ccg Pro	ctg Leu	ttc Phe 175	gcg Ala	528
atc Ile	ggt Gly	cct Pro	gcc Ala 180	att Ile	gtc Val	gaa Glu	gtc Val	ggg Gly 185	ggt Gly	acg Thr	aca Thr	ccc Pro	tta Leu 190	cca Pro	cag Gln	576
gat Asp	ggt Gly	aac Asn	ccg Pro	cgt Arg	cct Pro	cgc Arg	gta Val	ttc Phe	cga Arg	ctt Leu	cca Pro	tca Ser	cag Gln	aga Arg	gcg Ala	624
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atg Met	ata Ile 210	aac Asn	cgg Arg	tac Tyr	ggc Gly	ctc Leu 215	aac Asn	tcc Ser	aaa Lys	ggc Gly	gca Ala 220	gat Asp	cac His	atg Met	gca Ala	672
gct Ala 225	atc Ile	ttg Leu	gag Glu	caa Gln	cga Arg 230	gta Val	cgc Arg	gat Asp	ttt Phe	gcc Ala 235	tac Tyr	gca Ala	aac Asn	gga Gly	ttt Phe 240	720
ggg Gly	gca Ala	tac Tyr	gat Asp	gcg Ala 245	gct Ala	aag Lys	cag Gln	cgt Arg	gta Val 250	ttg Leu	gac Asp	ggc Gly	gaa Glu	gct Ala 255	ggt Gly	768
gtg Val	cca Pro	cca Pro	ggt Gly 260	agt Ser	ctt Leu	cag Gln	cct Pro	ggt Gly 265	aag Lys	ctt Leu	tta Leu	gct Ala 270	gtc Val	caa Gln	gtg Val	816
gca Ala	aag Lys	aac Asn 275	aag Lys	gcc Ala	act Thr	cct Pro	gac Asp 280	ggc Gly	gac Asp	att Ile	gaa Glu	gcc Ala 285	atc Ile	aag Lys	cgc Arg	864
gac Asp	tat Tyr 290	gtg Val	tat Tyr	tgc Cys	gtg Val	gac Asp 295	cgt Arg	gtg Val	gcc Ala	aaa Lys	tac Tyr 300	gct Ala	gat Asp	att Ile	ctt Leu	912
gtt Val 305	gtg Val	aat Asn	gta Val	tcg Ser	agc Ser 310	ccc Pro	aac Asn	aca Thr	ccc Pro	ggt Gly 315	ctc Leu	cgt Arg	gac Asp	ctt Leu	caa Gln 320	960
gcc Ala	act Thr	gcc Ala	ccg Pro	ctc Leu 325	aca Thr	gct Ala	atc Ile	ttg Leu 330	agt Ser	gct Ala	gtc Val	gtt Val	ggc Gly	gcg Ala 335	gca Ala	1008
aag Lys	agc Ser	gtg Val	aac Asn 340	cgc Arg	aag Lys	acc Thr	aaa Lys	cca Pro 345	tat Tyr	gtt Val	atg Met	gtc Val	aag Lys 350	gtc Val	agt Ser	1056
ccg Pro	gat Asp	gaa Glu 355	gac Asp	tca Ser	gat Asp	gaa Glu 360	caa Gln	gtc Val	tct Ser	ggt Gly	atc Ile	tgc Cys 365	gac Asp	gcc Ala	gtc Val	1104
cga Arg	gca Ala	tcc Ser	ggt Gly	gtc Val	gac Asp	gga Gly	gtg Val	att Ile	gtc Val	gga Gly	aac Asn	aca Thr	aca Thr	aac Asn	cgt Arg	1152

370	375	380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln 385 390 395 400			1200
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp 405 410 415			1248
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu 420 425 430			1296
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln 435 440 445			1344
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly 450 455 460			1392
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys 465 470 475 480			1440
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr 485 490 495			1488
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln 500 505 510			1536
gaa ctt cga acg gcg aaa aag gag Glu Leu Arg Thr Ala Lys Lys Glu 515 520			1560

<210> 28
 <211> 520
 <212> PRT
 <213> Aspergillus nidulans

<400> 28

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Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe	20	25	30	
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	35	40	45	
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys	50	55	60	
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu	65	70	75	80
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val	85	90	95	
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala	100	105	110	
Glu	Asp	Val	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	115	120	125	
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	130	135	140	
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	145	150	155	160
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	165	170	175	

Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln
			180					185					190		
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala
		195					200					205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala
	210					215					220				
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe
225				230						235					240
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly
			245						250					255	
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val
			260					265					270		
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
		275					280					285			
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
	290					295					300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
305				310						315					320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
			325					330						335	
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
			340					345					350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
		355					360				365				

Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
	370					375					380				
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
385				390						395					400
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
			405					410						415	
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
			420				425					430			
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
	435						440					445			
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
	450					455					460				
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
465				470						475					480
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
			485					490						495	
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
		500						505					510		
Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								
	515						520								

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 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (67)...(1611)
 <223> wild-type IMP dehydrogenase cDNA

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	Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro		
	1				5					10						
gac	gac	ggg	ctc	aca	gcg	cag	cag	ctc	ttc	aac	tgc	ggg	gac	ggc	ctc	156
Asp	Asp	Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	
	15				20					25					30	
acc	tac	aat	gat	ttt	ctc	att	ctt	cct	ggg	tat	atc	gac	ttc	act	gca	204
Thr	Tyr	Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	

35					40					45						
gat	cag	gtg	gac	ttg	acg	tct	gct	cta	act	aag	aag	att	aca	cta	aag	252
Asp	Gln	Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	
			50					55					60			
acc	cca	ttg	gtt	tcc	tca	ccc	atg	gac	act	gtc	aca	gag	gct	gga	atg	300
Thr	Pro	Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	
		65					70					75				
gcc	atc	gcg	atg	gcg	ctt	aca	gga	ggg	att	ggg	ttc	atc	cac	cac	aac	348
Ala	Ile	Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	
	80					85					90					
tgc	aca	cct	gaa	ttc	cag	gcc	aat	gaa	gtt	cgg	aaa	gtg	aag	aaa	tac	396
Cys	Thr	Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	
95					100					105					110	
gaa	cag	gga	ttc	atc	act	gac	ccc	gtg	gtc	ctt	agc	ccc	aag	gat	cgt	444
Glu	Gln	Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	
				115					120					125		
gta	cgc	gat	gtt	ttt	gag	gcc	aaa	gcc	agg	cat	ggc	ttc	tgt	ggg	atc	492
Val	Arg	Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	
			130					135					140			
ccc	atc	aca	gat	aca	ggc	cgg	atg	ggg	agt	cga	ttg	gtg	ggc	atc	atc	540
Pro	Ile	Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	
		145					150					155				
tcc	tca	agg	gac	att	gat	ttc	ctc	aag	gag	gaa	gag	cat	gac	cgg	ttc	588
Ser	Ser	Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	
	160					165						170				
ttg	gaa	gag	atc	atg	act	aag	agg	gaa	gat	ttg	gtg	gtc	gcc	cct	gcc	636
Leu	Glu	Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	
175					180					185					190	
ggc	gtc	act	ctg	aaa	gag	gca	aat	gag	att	ctg	cag	cga	agt	aaa	aag	684
Gly	Val	Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	
				195					200					205		
gga	aag	ttg	ccc	att	gtg	aat	gaa	aat	gat	gag	ctg	gta	gcc	atc	att	732
Gly	Lys	Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	
			210					215					220			
gcc	cgg	aca	gac	cta	aag	aag	aat	cgt	gat	tac	ccc	ctg	gcc	tcc	aaa	780
Ala	Arg	Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	
		225					230					235				
gat	gcc	aag	aag	caa	ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	828
Asp	Ala	Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	
	240					245					250					
gat	gac	aag	tat	agg	ctg	gac	tta	ctg	gcc	ctt	gct	ggg	gtg	gat	gta	876
Asp	Asp	Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	
255					260					265					270	
gtg	gtt	ttg	gac	tct	tcc	cag	gga	aac	tcc	atc	ttc	caa	atc	aat	atg	924
Val	Val	Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	
				275					280					285		
atc	aaa	tac	atc	aag	gag	aag	tat	ccc	agt	cta	cag	gtc	att	gga	ggc	972
Ile	Lys	Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	
			290					295					300			
aat	gta	gtc	act	gct	gcg	caa	gcc	aag	aac	ctc	ata	gat	gca	ggt	gta	1020

Asn	Val	Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	
	305						310					315				
gat	gct	ttg	cga	gtc	ggc	atg	gga	agt	ggg	tcc	atc	tgc	atc	acc	cag	1068
Asp	Ala	Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	
	320					325					330					
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Ser	Glu	Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	
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Ile	Gln	Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	
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Phe	Ser	Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	
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Val	Gln	Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	
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Ser	Ser	Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	
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Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
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Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
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acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca      204
Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala
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gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag      252
Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys
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gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac      348
Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn
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tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac      396
Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr
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gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt      444
Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg
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Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile
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ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc      540
Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile
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Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe
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Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala
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gag	tac	ttc	ttc	tca	gat	ggg	atc	cgg	ctg	aag	aaa	tac	cga	ggc	atg	1308				
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gtg	cag	gac	aag	ggg	tct	atc	cac	aag	ttc	gtt	cct	tac	ctg	att	gct	1452				
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Val	Arg	Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr		
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Lys	Arg	Leu	Phe	*													
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 <212> PRT
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Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro		
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Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln		
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Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys		
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Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala		
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Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp		
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Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys		
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Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val		
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Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala		
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Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
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Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
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Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly
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Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn
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Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val
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Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu
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Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro
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Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr
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Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu
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